

AMENDMENT TO THE SPECIFICATION:

Please amend paragraph [42] beginning at page 9 as follows:

[41] The gene expression data resulting from #4 are then spatially mapped onto the original multidimensional morphological matrix of image data. This is done by setting parameter bits in voxel data, to superimpose the expression message distribution upon the morphological volume image data. The volume image data is correlated with the x, y, z coordinates of the rasterized tissue samples so that ~~tissue samples~~ the locations of tissue samples are accurately located in the image data. This allows various types of analysis to be performed on the resultant correlated multidimensional spatial datasets. The details of implementing spatial mapping are well-known in the computer arts and not described in detail here.

[42] Some exemplary uses of the spatially mapped data will now be described. A researcher may desire information regarding mRNA synthesis at a particular location, expressed in x, y, z coordinates, of a tissue sample. A 3-dimensional view of the tissue would be displayed on the computer screen allowing the researcher to click on a voxel at the desired location. Techniques for creating an interactive 3-D volume visualization are described in the MultiVIS references described above. For example, as described in the MultiVIS paper, bits in the pixel displayed in the image can store the x,y,z coordinates of the pixel in the multidimensional spatial matrix of image data. These coordinates can be used to access the biological data obtained from analyzing the indexed incised sample section indexed by the same x,y,z coordinates. By clicking on a particular part of the image the biological data indexed in those pixels can be accessed. The mRNA synthesis data mapped to the voxel would be displayed in a variety of possible formats, e.g., as a table or a graph.